

IN THE CLAIMS

1-18 (cancelled)

19. (new) A method of producing double low restorer lines of *Brassica napus* for Ogura cytoplasmic male sterility (cms) presenting radish introgression carrying the *Rfo* restorer gene deleted of the radish *Pgi-2* allele and recombined with the *Pgi-2* gene from *Brassica oleracea*, and having a good agronomic value characterised by female fertility, a good transmission rate of *Rfo* and a high vegetative vigour, comprising:

a) crossing double low cms lines of spring *Brassica napus* comprising a deleted radish insertion with the double low line of spring Drakkar for forming heterozygous restored plants of *Brassica napus*;

b) irradiating before meiosis the heterozygous restored plants obtained in step a) with gamma ray irradiation;

c) crossing pollen from flowers obtained in step b) with the cms double low spring Wesroona line;

d) testing the progeny for vigour, female fertility and transmission rate of the cms gene; and

e) selecting progeny lines.

20. (new) The method of claim 19, wherein said irradiation dose in step b) is 65 Gray during 6 mn.

21. (new) The method of claim 19 wherein the double low cms line of spring *Brassica napus* of step a) is R211.

22. (new) The method of claim 19 wherein said testing is performed with the combination of five markers selected from the group consisting of PGIol, PGIUNT, PGIint, BolJon and CP418.

23. (new) Double low restorer lines of *Brassica napus* for Ogura cytoplasmic male sterility (cms) presenting an *Rfo* insertion deleted of the radish *Pgi-2* allele and recombined with the *Pgi-2* gene from *Brassica oleracea*, and having a good agronomic value characterised by female fertility, a good transmission rate of *Rfo* and a high vegetative vigour.

24. (new) The double low restorer lines of claim 23, wherein said lines present a unique combination of five markers selected from the group consisting of PGIol, PGIUNT, PGIint, BolJon and CP418.

25. (new) A method of producing *Brassica napus* hybrid plants and progeny thereof, comprising:

- a) providing a restorer line produced by the method of claim 19 and bred to be homozygous;
- b) using said restorer line in a hybrid production field as the pollinator;
- c) using cms sterile plants in a hybrid production field as the hybrid seed producing plant; and
- d) harvesting the hybrid seed from the male sterile plant.

26. (new) Seeds of *Brassica* plant developed from the *Brassica* line obtained by the method of claim 19.

27. (new) Seeds of *Brassica napus* obtained by the method of claim 25.

28. (new) Seeds of *Brassica napus* obtained by the method of claim 19 deposited in NCIMB Limited, under reference number NCIMB41183.

29. (new) A method for characterising recombined restorer lines of *Brassica napus* for Ogura cms presenting a *Rfo* insertion deleted of the radish *Pgi-2* allele and recombined with the *Pgi-2* gene from *Brassica oleracea*, and having a good agronomic value characterised by female fertility, a good transmission rate of *Rfo* and a high vegetative vigour, comprising the use of at least four markers, PGIol, PGIint, BolJon and CP418, or any portion of them containing at least one polymorphic site.

30. (new) The method of claim 29 wherein the combination of markers further comprises PGIUNT.

31. (new) The method of claim 30, wherein:

the marker PGIol is amplified using the primers: PGIol U, comprising SEQ ID NO:6 and PGIol L, comprising SEQ ID NO:7;

the marker PGIint is amplified using the primers: PGIint U, comprising SEQ ID NO:8 and PGIint L, comprising SEQ ID NO:9;

the marker BolJon is amplified using the primers: BolJon U, comprising SEQ ID NO:12 and BolJon L, comprising SEQ ID NO:13;

the marker CP418 is amplified using the primers: SG129 U, and pCP418 L, comprising SEQ ID NO: 14;

the marker PGIUNT is amplified using the primers: PGIol U, comprising SEQ ID NO:6 and PGIint L, comprising SEQ ID NO:9.

32. (new) A PGIol marker comprising SEQ ID NO:1.

33. (new) A PGIUNT marker comprising SEQ ID NO:2.

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- 34. (new) A PGIint marker comprising SEQ ID NO:3.
- 35. (new) A BolJon marker comprising SEQ ID NO:4.
- 36. (new) A CP418 marker comprising SEQ ID NO:5.